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<110> Dean, Nicholas M.
 Marcusson, Eric G.
 Wyatt, Jacqueline
 Zhang, Hong

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Gln Tyr Glu Thr Pro Phe Glu Gly Asn Leu Ile Asn Gln Glu Ile Met	
465 470 475	
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Thr Ile Cys Lys Asp Val Phe Asp Met Val Val Ala His Ile Gly Leu	
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Ser Phe Gly Pro Ser Gly Gly Leu Arg Glu Gly Ser Leu Ser Ser Gln	
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Asp Ser Arg Thr Glu Ser Ala Ser Leu Ser Gln Ser Gln Val Asn Gly	
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Gly Ser Pro Ser Pro Ser Val Ile Ser Lys Ala Thr Glu Lys Glu Thr	
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Phe Thr Asp Ser Asn Gln Ser Lys Thr Lys Lys Pro Gly Ile Ser Asp	
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Val Thr Asp Tyr Ser Asp Arg Gly Asp Ser Asp Met Asp Glu Ala Thr	
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Tyr Ser Ser Ser Gln Asp His Gln Thr Pro Lys Gln Glu Ser Ser Ser	
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Pro Pro Lys Pro Gly Asp Ile Phe Glu Val Glu Leu Ala Lys Asn Asp	
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Ser Asp Gly Arg Ile His Lys Gly Asp Arg Val Leu Ala Val Asn Gly	
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Val Ser Leu Glu Gly Ala Thr His Lys Gln Ala Val Glu Thr Leu Arg	
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Val Thr Ala Pro Ala Asn Ile Ser Asn Ser Thr Trp Ser Ser Ala Leu	
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His Gln Thr Leu Ser Asn Met Val Ser Gln Ala Gln Ser His His Glu	
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Ala Pro Lys Ser Gln Glu Asp Thr Ile Cys Thr Met Phe Tyr Tyr Pro	
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Ser Ala Ser Ser Ser Met Asp Lys Tyr His Ile His His Ile Ser	
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1760 1765 1770 1775	

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Ile Lys Ser Glu Lys Gly Ser Leu Gly Phe Thr Val Thr Lys Gly Asn	
1795 1800 1805	
cag aga att ggt tgt tat gtt cat gat gtc ata cag gat cca gcc aaa	5532
Gln Arg Ile Gly Cys Tyr Val His Asp Val Ile Gln Asp Pro Ala Lys	
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agt gat gga agg cta aaa cct ggg gac cgg ctc ata aag gtt aat gat	5580
Ser Asp Gly Arg Leu Lys Pro Gly Asp Arg Leu Ile Lys Val Asn Asp	
1825 1830 1835	
aca gat gtt act aat atg act cat aca gat gca gtt aat ctg ctc cgg	5628
Thr Asp Val Thr Asn Met Thr His Thr Asp Ala Val Asn Leu Leu Arg	
1840 1845 1850 1855	
gct gca tcc aaa aca gtc aga tta gtt att gga cga gtt cta gaa tta	5676
Ala Ala Ser Lys Thr Val Arg Leu Val Ile Gly Arg Val Leu Glu Leu	
1860 1865 1870	
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Pro Arg Ile Pro Met Leu Pro His Leu Leu Pro Asp Ile Thr Leu Thr	
1875 1880 1885	
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Cys Asn Lys Glu Glu Leu Gly Phe Ser Leu Cys Gly Gly His Asp Ser	
1890 1895 1900	
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1905 1910 1915	
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Ala Ile Glu Gly Asn Leu Gln Leu Leu Asp Val Ile His Tyr Val Asn	
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Gly Val Ser Thr Gln Gly Met Thr Leu Glu Glu Val Asn Arg Ala Leu	
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Pro Val Val Pro Ser Ser Lys Arg Ser Ala Val Ser Ala Pro Lys Ser	
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Thr Lys Gly Asn Gly Ser Tyr Ser Val Gly Ser Cys Ser Gln Pro Ala	
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Leu Thr Pro Asn Asp Ser Phe Ser Thr Val Ala Gly Glu Glu Ile Asn	
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Ser Pro Asn Leu Thr Leu Pro Lys Glu Ser Tyr Ile Gln Glu Asp Asp	
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Ile Tyr Asp Asp Ser Gln Glu Ala Glu Val Ile Gln Ser Leu Leu Asp	
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Val Val Asp Glu Glu Ala Gln Asn Leu Leu Asn Glu Asn Asn Ala Ala	
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Gly Tyr Ser Cys Gly Pro Gly Thr Leu Lys Met Asn Gly Lys Leu Ser	
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Glu Glu Arg Thr Glu Asp Thr Asp Cys Asp Gly Ser Pro Leu Pro Glu	
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Tyr Phe Thr Glu Ala Thr Lys Met Asn Gly Cys Glu Glu Tyr Cys Glu	
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Lys Pro Leu Asp Gln Cys Leu Ile Gly Gln Thr Lys Glu Asn Arg Arg	
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Lys Asn Arg Tyr Lys Asn Ile Leu Pro Tyr Asp Ala Thr Arg Val Pro	
2240 2245 2250 2255	

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Gln Arg Tyr Trp Pro Asn Ile Leu Gly Lys Thr Thr Met Val Ser Asn	
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Gln Pro Asp Asp Leu Leu Thr Phe Ile Ser Tyr Met Arg His Ile His	
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Gly Thr Leu Ile Cys Ile Asp Val Val Leu Gly Leu Ile Ser Gln Asp	
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Leu Asp Phe Asp Ile Ser Asp Leu Val Arg Cys Met Arg Leu Gln Arg	
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His Gly Met Val Gln Thr Glu Asp Gln Tyr Ile Phe Cys Tyr Gln Val	
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Ile Leu Tyr Val Leu Thr Arg Leu Gln Ala Glu Glu Glu Gln Lys Gln	
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Gln Pro Gln Leu Leu Lys	
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 <212> PRT
 <213> Homo sapiens

<400> 46

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Gln	Glu	Leu	Phe	Arg	Lys	Val	Ser	Leu	Ala	Asp	Pro	Ala	Ala	Leu	Gly
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Phe	Ile	Ile	Ser	Pro	Trp	Ser	Leu	Leu	Leu	Leu	Pro	Ser	Gly	Ser	Val
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Ser	Phe	Thr	Asp	Glu	Asn	Ile	Ser	Asn	Gln	Asp	Leu	Arg	Ala	Phe	Thr
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Ala	Pro	Glu	Val	Leu	Gln	Asn	Gln	Ser	Leu	Thr	Ser	Leu	Ser	Asp	Val
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Glu	Lys	Ile	His	Ile	Tyr	Ser	Leu	Gly	Met	Thr	Leu	Tyr	Trp	Gly	Ala
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Leu	Gly	Asn	Leu	Ser	Gly	Thr	Asp	Gln	Leu	Ser	Cys	Asn	Ser	Glu	Gln

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Lys	Pro	Asp	Arg	Ser	Gln	Ala	Ile	Arg	Asp	Arg	Leu	Arg	Gly	Lys	Gly																																								
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Leu	Pro	Thr	Gly	Arg	Ser	Ser	Thr	Ser	Asp	Val	Leu	Asp	Ile	Gln	Lys																																								
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Leu	Thr	Lys	Lys	Gly	Lys	Asn	Glu	Asp	Asn	Arg	Arg	Lys	Val	Asn	Ile	
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Pro	Glu	Lys	Lys	Ser	Gln	Thr	Gly	Ile	Leu	Leu	Gly	Val	Cys	Ser	Lys	
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2130	2135	2140
Asp Asp Asp Glu Ile Thr Trp Gly Asn Asp Glu Leu Pro Ile Glu Arg 145 2150 2155 2160		
Thr Asn His Glu Asp Ser Asp Lys Asp His Ser Phe Leu Thr Asn Asp 2165 2170 2175		
Glu Leu Ala Val Leu Pro Val Val Lys Val Leu Pro Ser Gly Lys Tyr 2180 2185 2190		
Thr Gly Ala Asn Leu Lys Ser Val Ile Arg Val Leu Arg Gly Leu Leu 2195 2200 2205		
Asp Gln Gly Ile Pro Ser Lys Glu Leu Glu Asn Leu Gln Glu Leu Lys 2210 2215 2220		
Pro Leu Asp Gln Cys Leu Ile Gly Gln Thr Lys Glu Asn Arg Arg Lys 225 2230 2235 2240		
Asn Arg Tyr Lys Asn Ile Leu Pro Tyr Asp Ala Thr Arg Val Pro Leu 2245 2250 2255		
Gly Asp Glu Gly Gly Tyr Ile Asn Ala Ser Phe Ile Lys Ile Pro Val 2260 2265 2270		
Gly Lys Glu Glu Phe Val Tyr Ile Ala Cys Gln Gly Pro Leu Pro Thr 2275 2280 2285		
Thr Val Gly Asp Phe Trp Gln Met Ile Trp Glu Gln Lys Ser Thr Val 2290 2295 2300		
Ile Ala Met Met Thr Gln Glu Val Glu Gly Glu Lys Ile Lys Cys Gln 305 2310 2315 2320		
Arg Tyr Trp Pro Asn Ile Leu Gly Lys Thr Thr Met Val Ser Asn Arg 2325 2330 2335		
Leu Arg Leu Ala Leu Val Arg Met Gln Gln Leu Lys Gly Phe Val Val 2340 2345 2350		
Arg Ala Met Thr Leu Glu Asp Ile Gln Thr Arg Glu Val Arg His Ile 2355 2360 2365		
Ser His Leu Asn Phe Thr Ala Trp Pro Asp His Asp Thr Pro Ser Gln 2370 2375 2380		
Pro Asp Asp Leu Leu Thr Phe Ile Ser Tyr Met Arg His Ile His Arg 385 2390 2395 2400		
Ser Gly Pro Ile Ile Thr His Cys Ser Ala Gly Ile Gly Arg Ser Gly 2405 2410 2415		
Thr Leu Ile Cys Ile Asp Val Val Leu Gly Leu Ile Ser Gln Asp Leu 2420 2425 2430		
Asp Phe Asp Ile Ser Asp Leu Val Arg Cys Met Arg Leu Gln Arg His 2435 2440 2445		
Gly Met Val Gln Thr Glu Asp Gln Tyr Ile Phe Cys Tyr Gln Val Ile 2450 2455 2460		

Leu Tyr Val Leu Thr Arg Leu Gln Ala Glu Glu Glu Gln Lys Gln Gln
 465 2470 2475 2480

Pro Gln Leu Leu Lys
 2485

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20

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<220>
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<400> 48
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20

<210> 49
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<400> 49
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20

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 gcaactcatc atttcccat 20

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 gctgccttta atcatcccta 20

<210> 64
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 <400> 64
 actggtttca agtatcccct 20

<210> 65
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 <304> 148
 <306> 1274-1297
 <307> 1992-02-15
 <308> M83649/Genbank
 <309> 1994-04-18
 <400> 65

gccgcaggct gccacacag gccgcccgt gttttccctt gctgcagac atg ctg tgg 58
 Met Leu Trp
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atc tgg gct gtc ctg cct ctg gtg ctt gct ggc tca cag tta aga gtt 106
 Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln Leu Arg Val
 5 10 15

cat act caa ggt act aat agc atc tcc gag agt tta aag ctg agg agg 154
 His Thr Gln Gly Thr Asn Ser Ile Ser Glu Ser Leu Lys Leu Arg Arg
 20 25 30 35

cgg gtt cat gaa act gat aaa aac tgc tca gaa gga tta tat caa gga 202
 Arg Val His Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu Tyr Gln Gly
 40 45 50

ggc cca ttt tgc tgt caa cca tgc caa cct ggt aaa aaa aaa gtt gag 250
 Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys Lys Val Glu
 55 60 65

gac tgc aaa atg aat ggg ggt aca cca acc tgt gcc cca tgc aca gaa 298
 Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro Cys Thr Glu
 70 75 80

ggg aag gag tac atg gac aag aac cat tat gct gat aaa tgc aga aga 346
 Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys Cys Arg Arg
 85 90 95

tgc aca ctc tgc gat gaa gag cat ggt tta gaa gtg gaa aca aac tgc 394
 Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu Thr Asn Cys
 100 105 110 115

acc ctg acc cag aat acc aag tgc aag tgc aaa cca gac ttc tac tgc 442
 Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp Phe Tyr Cys
 120 125 130

gat tct cct ggc tgt gaa cac tgt gtt cgc tgc gcc tcg tgt gaa cat 490
 Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser Cys Glu His
 135 140 145

gga acc ctt gag cca tgc aca gca acc agc aat aca aac tgc agg aaa 538
 Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn Cys Arg Lys
 150 155 160

caa agt ccc aga aat cgc cta tgg ttg ttg acc atc ctt gtt ttg tta 586
 Gln Ser Pro Arg Asn Arg Leu Trp Leu Leu Thr Ile Leu Val Leu Leu
 165 170 175

att cca ctt gta ttt ata tat cga aag tac cgg aaa aga aag tgc tgg 634
 Ile Pro Leu Val Phe Ile Tyr Arg Lys Tyr Arg Lys Arg Lys Cys Trp
 180 185 190 195

aaa agg aga cag gat gac cct gaa tct aga acc tcc agt cgt gaa acc 682
 Lys Arg Arg Gln Asp Asp Pro Glu Ser Arg Thr Ser Ser Arg Glu Thr
 200 205 210

ata cca atg aat gcc tca aat ctt agc ttg agt aaa tac atc ccg aga 730
 Ile Pro Met Asn Ala Ser Asn Leu Ser Leu Ser Lys Tyr Ile Pro Arg
 215 220 225

att gct gaa gac atg aca atc cag gaa gct aaa aaa ttt gct cga gaa 778
 Ile Ala Glu Asp Met Thr Ile Gln Glu Ala Lys Lys Phe Ala Arg Glu
 230 235 240

aat aac atc aag gag ggc aag ata gat gag atc atg cat gac agc atc 826
 Asn Asn Ile Lys Glu Gly Lys Ile Asp Glu Ile Met His Asp Ser Ile
 245 250 255

caa gac aca gct gag cag aaa gtc cag ctg ctc ctg tgc tgg tac caa 874
 Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Leu Cys Trp Tyr Gln
 260 265 270 275

tct cat ggg aag agt gat gca tat caa gat tta atc aag ggt ctc aaa 922
 Ser His Gly Lys Ser Asp Ala Tyr Gln Asp Leu Ile Lys Gly Leu Lys
 280 285 290

aaa gcc gaa tgt cgc aga acc tta gat aaa ttt cag gac atg gtc cag 970
 Lys Ala Glu Cys Arg Arg Thr Leu Asp Lys Phe Gln Asp Met Val Gln
 295 300 305

aag gac ctt gga aaa tca acc cca gac act gga aat gaa aat gaa gga 1018
 Lys Asp Leu Gly Lys Ser Thr Pro Asp Thr Gly Asn Glu Asn Glu Gly
 310 315 320

caa tgt ctg gag tga aaactacctc agttccagcc atgaagagag gagagagcct 1073
 Gln Cys Leu Glu
 325

gccacccatg atggaaacaa aatgaatgcc aactgtattg acattggcaa ctccctgggtgt 1133
 gttctctttg ccagcaaattg gtagttgata ctccagtgagg gtcaaattgac tagcagggttc 1193
 cagggactgc ttctgttatt ctctgcagtt gctgagatga accattttct ctgtctactg 1253
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 tttgtgttta tattcatata ctatgaactg aggagaatta taaactgaaa caaatactcg 1373
 cagttaattg aagaccttcc attgatggac agttcttttc ctctctatat ggaaatgtat 1433
 aatagaagaa ataattttta aattaaagta tctctttttg catttca 1480

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 <213> Mus musculus

<400> 66
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 Leu Arg Arg Arg Val His Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu
 35 40 45
 Tyr Gln Gly Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys
 50 55 60

Lys Val Glu Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro
 65 70 75 80
 Cys Thr Glu Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys
 85 90 95
 Cys Arg Arg Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu
 100 105 110
 Thr Asn Cys Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp
 115 120 125
 Phe Tyr Cys Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser
 130 135 140
 Cys Glu His Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn
 145 150 155 160
 Cys Arg Lys Gln Ser Pro Arg Asn Arg Leu Trp Leu Leu Thr Ile Leu
 165 170 175
 Val Leu Leu Ile Pro Leu Val Phe Ile Tyr Arg Lys Tyr Arg Lys Arg
 180 185 190
 Lys Cys Trp Lys Arg Arg Gln Asp Asp Pro Glu Ser Arg Thr Ser Ser
 195 200 205
 Arg Glu Thr Ile Pro Met Asn Ala Ser Asn Leu Ser Leu Ser Lys Tyr
 210 215 220
 Ile Pro Arg Ile Ala Glu Asp Met Thr Ile Gln Glu Ala Lys Lys Phe
 225 230 235 240
 Ala Arg Glu Asn Asn Ile Lys Glu Gly Lys Ile Asp Glu Ile Met His
 245 250 255
 Asp Ser Ile Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Leu Cys
 260 265 270
 Trp Tyr Gln Ser His Gly Lys Ser Asp Ala Tyr Gln Asp Leu Ile Lys
 275 280 285
 Gly Leu Lys Lys Ala Glu Cys Arg Arg Thr Leu Asp Lys Phe Gln Asp
 290 295 300
 Met Val Gln Lys Asp Leu Gly Lys Ser Thr Pro Asp Thr Gly Asn Glu
 305 310 315 320
 Asn Glu Gly Gln Cys Leu Glu
 325

<210> 67
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 <220>
 <223> Synthetic Sequence

<400> 67
 gcagcaaggg aaaacagcgg 20

<210> 68
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <220>
 <223> Synthetic Sequence

<400> 68
 ccacagcatg tctgcagcaa 20

<210> 69
 <211> 20
 <212> DNA
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<400> 69
 tttcatgaac ccgcctcctc 20

<210> 70
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<400> 70
 gggtcagggt gcagtttggt 20

<210> 71
 <211> 20
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 <213> Artificial Sequence
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<400> 71
 gaggcgcagc gaacacagtg 20

<210> 72
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<400> 72
 cataggcgat ttctgggact 20

<210> 73
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<400> 73
 tccagcactt tcttttccgg 20

<210> 74
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<400> 74
 ggtttcacga ctggaggttc 20

<210> 75
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 <212> DNA
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<400> 75
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<210> 76
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<400> 76
 gccctccttg atgttatattt 20

<210> 77
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<400> 77
ggtaccagca caggagcagc 20

<210> 78
<211> 20
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<400> 78
cggctttttt gagacccttg 20

<210> 79
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<400> 79
gtgtctgggg ttgattttcc 20

<210> 80
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<400> 80
tctcctctct tcatggctgg 20

<210> 81
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<400> 81
ggcattcatt ttgtttccat 20

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<400> 82
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<210> 83
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<400> 83
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<210> 84
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<400> 84
 gcagattcca cttcacattt 20

<210> 85
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<220>
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<400> 85
 aaggtcttca attaactgcg 20

<210> 86
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Antisense Oligonucleotide

<400> 86
 tccgtcatcg ctccctcaggg 20

<210> 87
 <211> 20
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<220>
 <223> Antisense Oligonucleotide

<400> 87

atgcattctg cccccaagga 20

<210> 88
 <211> 29
 <212> DNA
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<220>
 <223> PCR Primer

<400> 88
 tcatgacact aagtcaagtt aaaggcttt 29

<210> 89
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 89
 tcttggacat tgtcattctt gatctc 26

<210> 90
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Probe
 <400> 90
 attttggctt cattgacacc attctttcga a 31

<210> 91
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 91
 caacggattt ggtcgtattg g 21

<210> 92
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 92
 ggcaacaata tccactttac cagagt 26

<210> 93
 <211> 21
 <212> DNA
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<220>
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<400> 93
 cgctgtgtca ccagggctgc t

21

<210> 94
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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<400> 94
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 ttcacactca agagatactg attttgtcaa ttgtcctttc cccttttttt ctctcttccc 180
 tccttccatt ccttcttccc ttacctctcc tttccttccc tcacaccctt tttccttcc 240
 tctttttaca tttttttatt taaatgaact tttcattttg gaatagtttt aggatttcaa 300
 aaaatttgca gagataatac agagaatgcc catataccat cctccttata ccacttcttt 360
 ttgtgtctat tagatgctca gagtgtgtgc acaaggctgg cacaccaggt gtcttctca 420
 tggcactaac agtctactga aagggtggaac agagacaagc ctatcaacac ctacaagact 480
 ggtggttaagt gcagtgcag atgcaaaaca cagggatgat gaaagccctc aggagggtaa 540
 cctaacctag atttgagggc ccaaacaggc tccagaagaa aatgtcaact gagaggaagc 600
 ctgaaggatg aacagtgggc taagcaaagg gttattaatg tgttattaat gggttgaatc 660
 taattgggaa gggagagagg ttgcagagtg aggtgcagag cttggtggac gatgccaaag 720
 gaatactgaa acctttagtg tgtccagtct ggaactgcat ccaaattcag gttcagtaat 780
 gatgtcatta tccaaacata ctttctgtaa aattcatgct aaactaccta agagctatct 840
 accgttccaa agcaatagtg actttgaaca gtgttcacca gagcacgaaa gaattacaag 900
 attttttttt aaagaaaatt ggccaggaaa taatgagtaa cgaaggacag gaagtaattg 960
 tgaatgttta atatagctgg ggctatgcga tttggcttaa gttgttagct ttgttttcc 1020
 cttgagaaat aaaaactaag gggccctccc ttttcagagc cctatggcgc aacatctgta 1080

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ctttttcata tggttaactg tccattccag gaacgtctgt gagcctctca tgttgagacc 1140
acaacatgga cagcccagtc aaatgccccg caagtctttc tctgagtgac tccagcaatt 1200
agccaaggct cctgtaccca ggcaggacct ctgcgctctg agctccattc tccttcaaga 1260
cctccccaac ttcccagggt gaactacagc agaagccttt agaaagggca ggaggccggc 1320
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ccgcgcgcag gccaaagtgc tgaatcaatg gagccctccc caaccgggc gttccccagc 1500
gaggcttctt tcccatcctc ctgaccaccg gggcttttcg tgagctcgtc tctgatctcg 1560
cgcaagagtg acacacaggt gttcaaagac gcttctgggg agtgaggga gcggtttacg 1620
agtgacttgg ctggagcctc agggcggggc actggcacgg aacacaccct gagggccagcc 1680
ctggctgccc aggcggagct gcctcttctc ccgcgggttg gtggaccgc tcagtacgga 1740
gttggggaag ctctttcact tcggaggatt gctcaacaac c atg ctg ggc atc tgg 1796
                                     Met Leu Gly Ile Trp
                                     1           5

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acc ctc cta cct ctg gt gagccctctc ctgccgggt ggaggcttac cccgtcttag 1853
Thr Leu Leu Pro Leu
                        10

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tcccggggat aggcaaagtg gggcgggcgc gggacgcgtg cgggattgcg gcggcagcgg 1913
cgcacgcggg cacctgggag cggcgggctg ctgcgggagg cgttggagac tggctcccg 1973
gggctgttag gaccttcctt caggccccgg tgctcagaac gctggaggac ttgcttttct 2033
tgggccttga tgcgaagtgc tgaccccgct gggcaggcgg ggcagctccg gcgctcctcg 2093
gagaccactg cgctccacgt tgaggtgggc gtggggggcg gacaggaatt gaagcgggaag 2153
tctgggaagc tt 2165

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<210> 95
<211> 623
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (155)...(320)

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<400> 95
ctttcttgga gagagaaatc tgaaagacag tggagccctc acattgtctt tgctgtgca 60
cagcagatac tgccaatttt ggggtgggtta cactgggtta cacgttgctt acttcagaaa 120
tcaataaaat tctcttcatt cttttatttt acag gtt ctt acg tct gtt gct aga 175
                        Val Leu Thr Ser Val Ala Arg
                        1           i   5

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tta tcg tcc aaa agt gtt aat gcc caa gtg act gac atc aac tcc aag      223
Leu Ser Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser Lys
      10              15              20

gga ttg gaa ttg agg aag act gtt act aca gtt gag act cag aac ttg      271
Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn Leu
      25              30              35

gaa ggc ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca      319
Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro
      40              45              50              55

g gtatgttaca caaaacatcc agagattaca gtgaaagtc cagttaggag tagcacatag 380

taatcatgac tataataatt ttacagtttt tggttccctt atattatata acataactga 440

gagaaaaaca actatgaaat tattttccaa agatgagttt tatttatatt tatcatgctt 500

at ttgatgtg gttatggata aatttaattt acaagtgaca tgcacctctg aaatgagaag 560

actggtctat ttgggtccat ttttttctaa gcaaaaatga ctcat ttgtg aatatgaaag 620

ctt 623

<210> 96
<211> 924
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (146)...(283)

<400> 96
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ttattgtctg tcatccctct atacttccca ccctgttacc tgcccgtgtc ctgttcaaac      120

acttgctcct tttttccttg ggcag gtg aaa gga aag cta ggg act gca cag      172
          Val Lys Gly Lys Leu Gly Thr Ala Gln
          1              5

tca atg ggg atg aac cag act gcg tgc cct gcc aag aag gga agg agt      220
Ser Met Gly Met Asn Gln Thr Ala Cys Pro Ala Lys Lys Gly Arg Ser
      10              15              20              25

aca cag aca aag ccc att ttt ctt cca aat gca gaa gat gta gat tgt      268
Thr Gln Thr Lys Pro Ile Phe Leu Pro Asn Ala Glu Asp Val Asp Cys
          30              35              40

gtg atg aag gac atg gtaagagtct taaaatgcaa ttgaaagagg ccaatcttgg      323
Val Met Lys Asp Met
          45

aatttcatgt agaaccattt ataagacaat ttgaaattgg ggcctactgt ggtgctatgt      383

tgacacacag gaaaggggaag gacaggtggc taggggtaccg cagaaccagg tgccgagcta      443

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<222> (766)...(828)

<400> 98

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tgagtctcct gatcaccacc ggttgctaaa agtggcagcc tctaagggca gctgagtacc 120

ctccctgagc tacatcatgg gcgtggctat cacctggcca ttttcttggt ctataggaat 180
tttttgaaat tacttttgac agtttatttt aagagctagt ttaagctata ggatttacgt 240
gttcagttta ttactagggt taagtttatt tttgtatcca cttcatctct cttgtgtgtc 300
actattttcc tatcttcctt taactcttga aatcttaaga cagtcattcc ttatgatatt 360
tttcatccag ccatccaaat tatattaact tgtgccagct ttagatacta atttagaaat 420
atttgaagga atacgtttgc cagagatgca aagatgaata aaatggcccc taatttacia 480
agtgccattg aaaattataa aggaattatt ctgccaggct tttgaatttc tcctgtattt 540
ttttttctag atg tgt aca tgg aat cat caa gga atg cac act cac cag 589
          Met Cys Thr Trp Asn His Gln Gly Met His Thr His Gln
              1              5              10

caa cac caa gtg caa aga gga agg taattatttt tttacgggta tattctcctt 643
Gln His Gln Val Gln Arg Gly Arg
      15              20

tcccccaacc ccatggaaag atgtgaagaa aaaccaatca ctcttgatta gtagaaagtc 703
ctttatttaa tcttaaagat tgcttatttt catataaaat gtccaatggt ccaacctaca 763

gg atc cag atc tat ctt ggg gtg gct ttg tct tct tct ttt gcc aat 810
  Ile Gln Ile Tyr Leu Gly Val Ala Leu Ser Ser Ser Phe Ala Asn
      25              30              35

tcc act aat tgt ttg ggg taagttcttg ctttgttcaa actgcag 855
Ser Thr Asn Cys Leu Gly
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          Arg Glu Arg Lys Tyr Arg Lys His Ala Glu
              1              5              10

agc aca gaa agg aaa acc aag gtt ctc atg aat ctc caa cct tat atc 159
Ser Thr Glu Arg Lys Thr Lys Val Leu Met Asn Leu Gln Pro Tyr Ile
      15              20              25
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ct gtaggtattg aaataggtat cagctttcct tgaaaagaaa aatagagaaa 211
 ttagtgattt ggctttttgt tacttccttt tacttttttg tttcttggtt gtttcatttt 271
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 actgcag 338

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 gcttcctaatt tttatacatc aagcaactga ttgtacttct ttctgaatta aggaaaaatt 180
 agaagttcac atttagaata ttctaaagat atatttttat ttgtctttct ctgcttccat 240
 tttttgcttt ctag gaa aca gtg gca ata aat tta tct g gtaaggcttt 289
 Glu Thr Val Ala Ile Asn Leu Ser
 1 5
 tatcatttta tttcatagag atggcatcct ttagagtaat aggccaattt cagagtaaaa 349
 taatgttact aatttcagtg acatattatg ggatcttggt atttctcata cattctacct 409
 gctcagcata aagcatttat caggcagttt gtttaaattt ataatgagta ctcatagtta 469
 aaaataatca agtaacaata agacacaata gtctgaggct taagaaactt ttccttcata 529
 atcagctaga tgtattacag aactcctgcc taaaaagatc tagagggttaa agtgtactgt 589
 agactcaggt attatcagtg taccctaactc tataacaaca tacatgattc cattcagtgg 649
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Met Leu Thr Cys Val Asn Ile	
1 5	
tca cca cta ttg ctg gag tca tgt cac tat gtc aag tta aag gct ttg	163
Ser Pro Leu Leu Leu Glu Ser Cys His Tyr Val Lys Leu Lys Ala Leu	
10 15 20	
ttc gaa aga atg gtg tca atg aag cca aaa tag atg aga tca aga atg	211
Phe Glu Arg Met Val Ser Met Lys Pro Lys Met Arg Ser Arg Met	
25 30 35	
aca atg tcc aag aca cag cag aac aga aag ttc aac tgc ttc gta att	259
Thr Met Ser Lys Thr Gln Gln Asn Arg Lys Phe Asn Cys Phe Val Ile	
40 45 50 55	
ggc atc aac ttc atg gaa aga aag aag cgt atg aca cat tga tta aag	307
Gly Ile Asn Phe Met Glu Arg Lys Lys Arg Met Thr His Leu Lys	
60 65 70	
atc tca aaa aag cca atc ttt gta ctc ttg cag aga aaa ttc aga cta	355
Ile Ser Lys Lys Pro Ile Phe Val Leu Leu Gln Arg Lys Phe Arg Leu	
75 80 85	
tca tcc tca agg aca tta cta gtg act cag aaa att caa act tca gaa	403
Ser Ser Ser Arg Thr Leu Leu Val Thr Gln Lys Ile Gln Thr Ser Glu	
90 95 100	
atg aaa tcc aaa gct tgg tct ag agtgaaaaac aacaaattca gttctgagta	456
Met Lys Ser Lys Ala Trp Ser	
105 110	
tatgcaatta gtgtttgaaa agattcttaa tagctggctg taaatactgc ttggtttttt	516
actgggtaca ttttatcatt tattagcgct gaagagccaa catatttgta gatttttaaat	576
atctcatgat tctgectcca aggatgttta aaatctagtt gggaaaacaa acttcatcaa	636
gagtaaatgc agtggcatgc taagtaccca aataggagtg tatgcagagg atgaaagatt	696
aagattatgc tctggcatct aacatatgat tctgtagtat gaatgtaatc agtgtatggt	756
agtacaaatg tctatccaca ggctaacccc actctatgaa tcaatagaag aagctatgac	816
cttttgctga aatatcagtt actgaacagg caggccactt tgcctctaaa ttacctctga	876
taattctaga gattttacca tattttctaaa ctttgtttat aactctgaga agatcatatt	936
tatgtaaagt atatgtatgt gagtgcagaa tttaaataag gctctacctc aaagaccttt	996
gcacagttta ttggtgtcat attatacaat atttcaattg tgaattcaca tagaaaacat	1056
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tctccatttt tgccttggtg ctcactctaa tggcctaattg ccccccaaa catggaaata	1236
tcaccaaaaa atacttaata gtccacaaa aggcaagact gcccttagaa attctagcct	1296

ggtttggaga tactaactgc tctcagagaa agtagctttg tgacatgtca tgaacccatg 1356
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 1 5 10 15
 aga tta tcg tcc aaa agt gtt aat gcc caa gtg act gac atc aac tcc 96
 Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
 20 25 30
 aag gga ttg gaa ttg agg aag act gtt act aca gtt gag act cag aac 144
 Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
 35 40 45
 ttg gaa ggc ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct 192
 Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
 50 55 60
 cca ggt gaa agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca 240
 Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
 65 70 75 80
 gac tgc gtg ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat 288
 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
 85 90 95
 ttt tct tcc aaa tgc aga aga tgt aga ttg tgt gat gaa gga cat gat 336
 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Asp
 100 105 110
 gtg aac atg gaa tca tca agg aat gca cac tca cca gca aca cca agt 384
 Val Asn Met Glu Ser Ser Arg Asn Ala His Ser Pro Ala Thr Pro Ser
 115 120 125

gca aag agg aag tga agagaaagga agtacagaaa acatgcagaa agcacagaaa 439
 Ala Lys Arg Lys
 130

ggaaaaccaa ggttctcatg aatctccaac cttaaattcct gaaacagtgg caataaattt 499
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 agttaaaggc tttgttcgaa agaattggtgt caatgaagcc aaaatagatg agatcaagaa 619
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 tcatggaaag aaagaagcgt atgacacatt gattaaagat ctcaaaaaag ccaatctttg 739
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